



ENTERED PCT10

RAW SEQUENCE LISTING

DATE: 03/21/2002

PATENT APPLICATION: US/10/070,789

TIME: 15:43:31

Input Set : A:\Sequence

Output Set: N:\CRF3\03212002\J070789.raw

```

5 <110> APPLICANT: C. Frank Bennett
6   Elizabeth J. Ackermann
7   Lex M. Cowsert
8   ISIS PHARMACEUTICALS, INC.
10 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS
EXPRESSION
12 <130> FILE REFERENCE: RTSP-0048
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/070,789
C--> 14 <141> CURRENT FILING DATE: 2002-03-08
14 <150> PRIOR APPLICATION NUMBER: US 09/392,580
15 <151> PRIOR FILING DATE: 1999-09-09
17 <160> NUMBER OF SEQ ID NOS: 47
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2540
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (34)..(1527)
28 <400> SEQUENCE: 1
29   gaaaagggtgg acaagtccta ttttcaagag aag atg act ttt aac agt ttt      51
30                               Met Thr Phe Asn Ser Phe
31                               1           5
33   gaa gga tct aaa act tgt gta cct gca gac atc aat aag gaa gaa gaa      99
34   Glu Gly Ser Lys Thr Cys Val Pro Ala Asp Ile Asn Lys Glu Glu Glu
35           10           15           20
37   ttt gta gaa gag ttt aat aga tta aaa act ttt gct aat ttt cca agt      147
38   Phe Val Glu Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser
39           25           30           35
41   ggt agt cct gtt tca gca tca aca ctg gca cga gca ggg ttt ctt tat      195
42   Gly Ser Pro Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr
43           40           45           50
45   act ggt gaa gga gat acc gtg cgg tgc ttt agt tgt cat gca gct gta      243
46   Thr Gly Glu Gly Asp Thr Val Arg Cys Phe Ser Cys His Ala Ala Val
47           55           60           65           70
49   gat aga tgg caa tat gga gac tca gca gtt gga aga cac agg aaa gta      291
50   Asp Arg Trp Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Lys Val
51           75           80           85
53   tcc cca aat tgc aga ttt atc aac ggc ttt tat ctt gaa aat agt gcc      339
54   Ser Pro Asn Cys Arg Phe Ile Asn Gly Phe Tyr Leu Glu Asn Ser Ala
55           90           95           100
56   acg cag tct aca aat tct ggt atc cag aat ggt cag tac aaa gtt gaa      387
57   Thr Gln Ser Thr Asn Ser Gly Ile Gln Asn Gly Gln Tyr Lys Val Glu
58           105           110           115

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60	aac tat ctg gga agc aga gat cat ttt gcc tta gac agg cca tct gag	435
61	Asn Tyr Leu Gly Ser Arg Asp His Phe Ala Leu Asp Arg Pro Ser Glu	
62	120 125 130	
64	aca cat gca gac tat ctt ttg aga act ggg cag gtt gta gat ata tca	483
65	Thr His Ala Asp Tyr Leu Leu Arg Thr Gly Gln Val Val Asp Ile Ser	
66	135 140 145 150	
68	gac acc ata tac ccg agg aac cct gcc atg tat tgt gaa gaa gct aga	531
69	Asp Thr Ile Tyr Pro Arg Asn Pro Ala Met Tyr Cys Glu Glu Ala Arg	
70	155 160 165	
72	tta aag tcc ttt cag aac tgg cca gac tat gct cac cta acc cca aga	579
73	Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His Leu Thr Pro Arg	
74	170 175 180	
76	gag tta gca agt gct gga ctc tac tac aca ggt att ggt gac caa gtg	627
77	Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ile Gly Asp Gln Val	
78	185 190 195	
80	cag tgc ttt tgt tgt ggt gga aaa ctg aaa aat tgg gaa cct tgt gat	675
81	Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp Glu Pro Cys Asp	
82	200 205 210	
84	cgt gcc tgg tca gaa cac agg cga cac ttt cct aat tgc ttc ttt gtt	723
85	Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn Cys Phe Phe Val	
86	215 220 225 230	
88	ttg ggc cgg aat ctt aat att cga agt gaa tct gat gct gtg agt tct	771
89	Leu Gly Arg Asn Leu Asn Ile Arg Ser Glu Ser Asp Ala Val Ser Ser	
90	235 240 245	
92	gat agg aat ttc cca aat tca aca aat ctt cca aga aat cca tcc atg	819
93	Asp Arg Asn Phe Pro Asn Ser Thr Asn Leu Pro Arg Asn Pro Ser Met	
94	250 255 260	
96	gca gat tat gaa gca cgg atc ttt act ttt ggg aca tgg ata tac tca	867
97	Ala Asp Tyr Glu Ala Arg Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser	
98	265 270 275	
100	gtt aac aag gag cag ctt gca aga gct gga ttt tat gct tta ggt gaa	915
101	Val Asn Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu	
102	280 285 290	
104	ggt gat aaa gta aag tgc ttt cac tgt gga gga ggg cta act gat tgg	963
105	Gly Asp Lys Val Lys Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp	
106	295 300 305 310	
108	aag ccc agt gaa gac cct tgg gaa caa cat gct aaa tgg tat cca ggg	1011
109	Lys Pro Ser Glu Asp Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly	
110	315 320 325	
112	tgc aaa tat ctg tta gaa cag aag gga caa gaa tat ata aac aat att	1059
113	Cys Lys Tyr Leu Leu Glu Gln Lys Gly Gln Glu Tyr Ile Asn Asn Ile	
114	330 335 340	
116	cat tta act cat tca ctt gag gag tgt ctg gta aga act act gag aaa	1107
117	His Leu Thr His Ser Leu Glu Glu Cys Leu Val Arg Thr Thr Glu Lys	
118	345 350 355	
120	aca cca tca cta act aga aga att gat gat acc atc ttc caa aat cct	1155
121	Thr Pro Ser Leu Thr Arg Arg Ile Asp Asp Thr Ile Phe Gln Asn Pro	
122	360 365 370	
124	atg gta caa gaa gct ata cga atg ggg ttc agt ttc aag gac att aag	1203

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```

125   Met Val Gln Glu Ala Ile Arg Met Gly Phe Ser Phe Lys Asp Ile Lys
126   375                               380                               385                               390
128   aaa ata atg gag gaa aaa att cag ata tct ggg agc aac tat aaa tca      1251
129   Lys Ile Met Glu Glu Lys Ile Gln Ile Ser Gly Ser Asn Tyr Lys Ser
130                               395                               400                               405
132   ctt gag gtt ctg gtt gca gat cta gtg aat gct cag aaa gac agt atg      1299
133   Leu Glu Val Leu Val Ala Asp Leu Val Asn Ala Gln Lys Asp Ser Met
134                               410                               415                               420
136   caa gat gag tca agt cag act tca tta cag aaa gag att agt act gaa      1347
137   Gln Asp Glu Ser Ser Gln Thr Ser Leu Gln Lys Glu Ile Ser Thr Glu
138                               425                               430                               435
140   gag cag cta agg cgc ctg caa gag gag aag ctt tgc aaa atc tgt atg      1395
141   Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Cys Lys Ile Cys Met
142   440                               445                               450
144   gat aga aat att gct atc gtt ttt gtt cct tgt gga cat cta gtc act      1443
145   Asp Arg Asn Ile Ala Ile Val Phe Val Pro Cys Gly His Leu Val Thr
146   455                               460                               465                               470
148   tgt aaa caa tgt gct gaa gca gtt gac aag tgt ccc atg tgc tac aca      1491
149   Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys Tyr Thr
150                               475                               480                               485
152   gtc att act ttc aag caa aaa att ttt atg tct taa tctaactcta      1537
153   Val Ile Thr Phe Lys Gln Lys Ile Phe Met Ser
154                               490                               495
156   tagtaggcat gttatgttgt tcttattacc ctgattgaat gtgtgatgtg aactgacttt      1597
158   aagtaatcag gattgaattc cattagcatt tgctaccaag taggaaaaaa aatgtacatg      1657
160   gcagtgtttt agttggcaat ataacttttg aatttcttga tttttcaggg tattagctgt      1717
162   attatccatt ttttttactg ttattttaatt gaaaccatag actaagaata agaagcatca      1777
164   tactataact gaacacaatg tgtattcata gtatactgat ttaatttcta agtgtaagtg      1837
166   aattaatcat ctggattttt tattcttttc agataggctt aacaaatgga gctttctgta      1897
168   tataaatgtg gagattagag ttaatctccc caatcacata atttgttttg tgtgaaaaag      1957
170   gaataaattg ttccatgctg gtggaaagat agagattgtt tttagagggtt ggttggtgtg      2017
172   ttttaggatt ctgtccattt tcttgtaaag ggataaacac ggacgtgtgc gaaatatgtt      2077
174   tgtaaaagtga tttgccattg ttgaaagcgt atttaatgat agaatactat cgagccaaca      2137
176   tgtactgaca tggaaagatg tcagagatat gttaagtgtg aaatgcaagt ggcgggacac      2197
178   tatgtatagt ctgagccaga tcaaagtatg tatgttggtg atatgcatag aacgagagat      2257
180   ttggaaagat atacaccaaa ctgttaaagt tggtttctct tcggggaggg ggggattggg      2317
182   ggagggggccc cagagggggt ttagaggggc cttttcactt tcgacttttt tcattttgtt      2377
184   ctgttcggat tttttataag tatgtagacc ccgaagggtt ttatgggaac taacatcagt      2437
186   aacctaacc cctgtactat cctgtgctct tcctagggag ctgtgttggt tcccaccac      2497
188   caccctccc tctgaacaaa tgcctgagtg ctggggcact ttg                               2540
191 <210> SEQ ID NO: 2
192 <211> LENGTH: 24
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
W--> 196 <220> FEATURE:
      196 <223> OTHER INFORMATION: PCR Primer
      198 <400> SEQUENCE: 2
      199   ttccaagtgg tagtcctgtt tcag
      202 <210> SEQ ID NO: 3

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203 <211> LENGTH: 23
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
W--> 207 <220> FEATURE:
207 <223> OTHER INFORMATION: PCR Primer
209 <400> SEQUENCE: 3
210      gcacggtatc tccttcacca gta                                23
213 <210> SEQ ID NO: 4
214 <211> LENGTH: 27
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
W--> 218 <220> FEATURE:
218 <223> OTHER INFORMATION: PCR Probe
220 <400> SEQUENCE: 4
221      caacactggc acgagcaggg tttcttt                                27
224 <210> SEQ ID NO: 5
225 <211> LENGTH: 19
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
W--> 229 <220> FEATURE:
229 <223> OTHER INFORMATION: PCR Primer
231 <400> SEQUENCE: 5
232      gaaggtgaag gtcggagtc                                19
235 <210> SEQ ID NO: 6
236 <211> LENGTH: 20
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
W--> 240 <220> FEATURE:
240 <223> OTHER INFORMATION: PCR Primer
242 <400> SEQUENCE: 6
243      gaagatggtg atgggatttc                                20
246 <210> SEQ ID NO: 7
247 <211> LENGTH: 20
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
W--> 251 <220> FEATURE:
251 <223> OTHER INFORMATION: PCR Probe
253 <400> SEQUENCE: 7
254      caagcttccc gttctcagcc                                20
257 <210> SEQ ID NO: 8
258 <211> LENGTH: 20
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial Sequence
W--> 262 <220> FEATURE:
262 <223> OTHER INFORMATION: Antisense Oligonucleotide
264 <400> SEQUENCE: 8
265      taggacttgt ccaccttttc                                20
268 <210> SEQ ID NO: 9
269 <211> LENGTH: 20

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270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
W--> 273 <220> FEATURE:
273 <223> OTHER INFORMATION: Antisense Oligonucleotide
275 <400> SEQUENCE: 9
276     ttgaaaaatag gacttgtcca                                20
279 <210> SEQ ID NO: 10
280 <211> LENGTH: 20
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
W--> 284 <220> FEATURE:
284 <223> OTHER INFORMATION: Antisense Oligonucleotide
286 <400> SEQUENCE: 10
287     tcttctcttg aaaaataggac                                20
290 <210> SEQ ID NO: 11
291 <211> LENGTH: 20
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
W--> 295 <220> FEATURE:
295 <223> OTHER INFORMATION: Antisense Oligonucleotide
297 <400> SEQUENCE: 11
298     catcttctct tgaaaaatagg                                20
301 <210> SEQ ID NO: 12
302 <211> LENGTH: 20
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial Sequence
W--> 306 <220> FEATURE:
306 <223> OTHER INFORMATION: Antisense Oligonucleotide
308 <400> SEQUENCE: 12
309     gtcacatctt cttgaaaaata                                20
312 <210> SEQ ID NO: 13
313 <211> LENGTH: 20
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
W--> 317 <220> FEATURE:
317 <223> OTHER INFORMATION: Antisense Oligonucleotide
319 <400> SEQUENCE: 13
320     aagtcacatt ctcttgaaaa                                20
323 <210> SEQ ID NO: 14
324 <211> LENGTH: 20
325 <212> TYPE: DNA
326 <213> ORGANISM: Artificial Sequence
W--> 328 <220> FEATURE:
328 <223> OTHER INFORMATION: Antisense Oligonucleotide
330 <400> SEQUENCE: 14
331     aaaagtcac ttctcttgaa                                20
334 <210> SEQ ID NO: 15
335 <211> LENGTH: 20
336 <212> TYPE: DNA

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VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:196 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:207 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:218 M:258 W: Mandatory Feature missing, <220> FEATURE:
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